

cag	atg	att	gtt	cat	cct	acc	ccc	acg	cca	² atc	cgt	gca	ggc	gat	ggc	486
Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
				140					145					150		
cac	cgg	cta	acc	ctg	gaa	gac	atc	ttc	cat	gac	ctg	ttc	tac	cac	tta	534
His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
			155					160					165			
gag	ctc	cag	gtc	aac	cgc	acc	tac	caa	atg	cac	ctt	gga	ggg	aag	cag	582
Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
		170					175					180				
aga	gaa	tat	gag	ttc	ttc	ggc	ctg	acc	cct	gac	aca	gag	ttc	ctt	ggc	630
Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	
	185					190					195					
acc	atc	atg	att	tgc	gtt	ccc	acc	tgg	gcc	aag	gag	agt	gcc	ccc	tac	678
Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	
200				205						210					215	
atg	tgc	cga	gtg	aag	aca	ctg	cca	gac	cgg	aca	tgg	acc	tac	tcc	ttc	726
Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
				220					225					230		
tcc	gga	gcc	ttc	ctg	ttc	tcc	atg	ggc	ttc	ctc	gtc	gca	gta	ctc	tgc	774
Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys	
			235					240					245			
tac	ctg	agc	tac	aga	tat	gtc	acc	aag	ccg	cct	gca	cct	ccc	aac	tcc	822
Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser	
		250					255					260				
ctg	aac	gtc	cag	cga	gtc	ctg	act	ttc	cag	ccg	ctg	cgc	ttc	atc	cag	870
Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln	
	265					270					275					
gag	cac	gtc	ctg	atc	cct	gtc	ttt	gac	ctc	agc	ggc	ccc	agc	agt	ctg	918
Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu	
280					285					290					295	
gcc	cag	cct	gtc	cag	tac	tcc	cag	atc	agg	gtg	tct	gga	ccc	agg	gag	966
Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile	Arg	Val	Ser	Gly	Pro	Arg	Glu	
				300					305					310		
ccc	gca	gga	gct	cca	cag	cgg	cat	agc	ctg	tcc	gag	atc	acc	tac	tta	1014
Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser	Leu	Ser	Glu	Ile	Thr	Tyr	Leu	
			315					320					325			
ggg	cag	cca	gac	atc	tcc	atc	ctc	cag	ccc	tcc	aac	gtg	cca	cct	ccc	1062
Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln	Pro	Ser	Asn	Val	Pro	Pro	Pro	
		330					335					340				
cag	atc	ctc	tcc	cca	ctg	tcc	tat	gcc	cca	aac	gct	gcc	cct	gag	gtc	1110
Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala	Pro	Asn	Ala	Ala	Pro	Glu	Val	
	345					350					355					
ggg	ccc	cca	tcc	tat	gca	cct	cag	gtg	acc	ccc	gaa	gct	caa	ttc	cca	1158
Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val	Thr	Pro	Glu	Ala	Gln	Phe	Pro	
360					365					370					375	
ttc	tac	gcc	cca	cag	gcc	atc	tct	aag	gtc	cag	cct	tcc	tcc	tat	gcc	1206
Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	Val	Gln	Pro	Ser	Ser	Tyr	Ala	
				380					385					390		
cct	caa	gcc	act	ccg	gac	agc	tgg	cct	ccc	tcc	tat	ggg	gta	tgc	atg	1254
Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro	Pro	Ser	Tyr	Gly	Val	Cys	Met	
			395					400					405			
gaa	ggt	tct	ggc	aaa	gac	tcc	ccc	act	ggg	aca	ctt	tct	agt	cct	aaa	1302

Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	Gly	Thr	Leu	Ser	Ser	Pro	Lys	
410							415					420				
cac	ctt	agg	cct	aaa	ggt	cag	ctt	cag	aaa	gag	cca	cca	gct	gga	agc	1350
His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln	Lys	Glu	Pro	Pro	Ala	Gly	Ser	
425						430					435					
tgc	atg	tta	ggt	ggc	ctt	tct	ctg	cag	gag	gtg	acc	tcc	ttg	gct	atg	1398
Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln	Glu	Val	Thr	Ser	Leu	Ala	Met	
440					445					450					455	
gag	gaa	tcc	caa	gaa	gca	aaa	tca	ttg	cac	cag	ccc	ctg	ggg	att	tgc	1446
Glu	Glu	Ser	Gln	Glu	Ala	Lys	Ser	Leu	His	Gln	Pro	Leu	Gly	Ile	Cys	
			460						465					470		
aca	gac	aga	aca	tct	gac	cca	aat	gtg	cta	cac	agt	ggg	gag	gaa	ggg	1494
Thr	Asp	Arg	Thr	Ser	Asp	Pro	Asn	Val	Leu	His	Ser	Gly	Glu	Glu	Gly	
			475					480					485			
aca	cca	cag	tac	cta	aag	ggc	cag	ctc	ccc	ctc	ctc	tcc	tca	gtc	cag	1542
Thr	Pro	Gln	Tyr	Leu	Lys	Gly	Gln	Leu	Pro	Leu	Leu	Ser	Ser	Val	Gln	
		490				495						500				
atc	gag	ggc	cac	ccc	atg	tcc	ctc	cct	ttg	caa	cct	cct	tcc	ggt	cca	1590
Ile	Glu	Gly	His	Pro	Met	Ser	Leu	Pro	Leu	Gln	Pro	Pro	Ser	Gly	Pro	
	505					510					515					
tgt	tcc	ccc	tcg	gac	caa	ggt	cca	agt	ccc	tgg	ggc	ctg	ctg	gag	tcc	1638
Cys	Ser	Pro	Ser	Asp	Gln	Gly	Pro	Ser	Pro	Trp	Gly	Leu	Leu	Glu	Ser	
520					525					530					535	
ctt	gtg	tgt	ccc	aag	gat	gaa	gcc	aag	agc	cca	gcc	cct	gag	acc	tca	1686
Leu	Val	Cys	Pro	Lys	Asp	Glu	Ala	Lys	Ser	Pro	Ala	Pro	Glu	Thr	Ser	
				540					545					550		
gac	ctg	gag	cag	ccc	aca	gaa	ctg	gat	tct	ctt	ttc	aga	ggc	ctg	gcc	1734
Asp	Leu	Glu	Gln	Pro	Thr	Glu	Leu	Asp	Ser	Leu	Phe	Arg	Gly	Leu	Ala	
			555					560					565			
ctg	act	gtg	cag	tgg	gag	tcc	tgaggggaat	gggaaaggct	tggtgcttcc							1785
Leu	Thr	Val	Gln	Trp	Glu	Ser										
		570														

tccctgtccc	tacccagtgt	cacatccttg	gctgtcaatc	ccatgcctgc	ccatgccaca	1845
cactctgcga	tctggcctca	gacgggtgcc	cttgagagaa	gcagagggag	tggcatgcag	1905
ggccccctgcc	atgggtgcgc	tcctcaccgg	aacaaagcag	catgataagg	actgcagcgg	1965
gggagctctg	gggagcagct	tgtgtagaca	agcgcgtgct	cgctgagccc	tgcaaggcag	2025
aaatgacagt	gcaaggagga	aatgcaggga	aactcccagag	gtccagagcc	ccacctccta	2085
acaccatgga	ttcaaagtgc	tcagggaatt	tgcctctcct	tgccccattc	ctggccagtt	2145
tcacaatcta	gctcgacaga	gcatgaggcc	cctgcctctt	ctgtcattgt	tcaaagggtg	2205
gaagagagcc	tggaaaagaa	ccaggcctgg	aaaagaacca	gaaggaggct	gggcagaacc	2265
agaacaacct	gcacttctgc	caaggccagg	gccagcagga	cggcaggact	ctagggaggg	2325
gtgtggcctg	cagctcattc	ccagccaggg	caactgcctg	acgttgacag	atttcagctt	2385
cattcctctg	atagaacaaa	gcgaaatgca	ggtccaccag	ggagggagac	acacaagcct	2445
tttctgcagg	caggagtctc	agaccctatc	ctgagaatgg	ggtttgaaag	gaagggtgag	2505
gctgtggccc	ctggacgggt	acaataacac	actgtactga	tgtcacaact	ttgcaagctc	2565
tgccttgggt	tcagcccatc	tgggctcaaa	ttccagcctc	accactcaca	agctgtgtga	2625
cttcaaacaa	atgaaatcag	tgcccagaac	ctcggtttcc	tcactctgtaa	tgtggggatc	2685
ataaacaccta	cctcatggag	ttgtggtgaa	gatgaaatga	agtcattgtct	ttaaagtgc	2745
taatagtgcc	tggtacatgg	gcagtgccca	ataaacggta	gctattttaa	aaaaaaaaaa	2805
aaaaaaaaaa	atagcggccg	cctcga				2831

<210> 2
 <211> 574
 <212> PRT
 <213> Homo sapien

<400> 2
 Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His

1	5	10	4	15
Ala Pro Glu Asp	Pro Ser Asp Leu	Leu Gln His Val Lys	Phe Gln Ser	
Ser Asn Phe	Asn Ile Leu Thr	Trp Asp Ser Gly	Pro Glu Gly Thr	
Pro Asp Thr	Val Tyr Ser Ile	Glu Tyr Lys Thr Tyr	Gly Glu Arg Asp	
Trp Val Ala	Lys Lys Gly Cys	Gln Arg Ile Thr Arg	Lys Ser Cys Asn	
Leu Thr Val	Glu Thr Gly Asn	Leu Thr Glu Tyr Tyr	Ala Arg Val	
Thr Ala Val	Ser Ala Gly Gly	Arg Ser Ala Thr Lys	Met Thr Asp Arg	
Phe Ser Ser	Leu Gln His Thr	Thr Leu Lys Pro Pro	Asp Val Thr Cys	
Ile Ser Lys	Val Arg Ser Ile	Gln Met Ile Val His	Pro Thr Pro Thr	
Pro Ile Arg	Ala Gly Asp Gly	His Arg Leu Thr	Leu Glu Asp Ile Phe	
His Asp Leu	Phe Tyr His Leu	Glu Leu Gln Val Asn	Arg Thr Tyr Gln	
Met His Leu	Gly Gly Lys Gln	Arg Glu Tyr Glu	Phe Phe Gly Leu Thr	
Pro Asp Thr	Glu Phe Leu Gly	Thr Ile Met Ile Cys	Val Pro Thr Trp	
Ala Lys Glu	Ser Ala Pro Tyr	Met Cys Arg Val Lys	Thr Leu Pro Asp	
Arg Thr Trp	Thr Tyr Ser Phe	Ser Gly Ala Phe	Leu Phe Ser Met Gly	
Phe Leu Val	Ala Val Leu Cys	Tyr Leu Ser Tyr	Arg Tyr Val Thr Lys	
Pro Pro Ala	Pro Pro Asn Ser	Leu Asn Val Gln	Arg Val Leu Thr Phe	
Gln Pro Leu	Arg Phe Ile Gln	Glu His Val Leu	Ile Pro Val Phe Asp	
Leu Ser Gly	Pro Ser Ser Leu	Ala Gln Pro Val	Gln Tyr Ser Gln Ile	
Arg Val Ser	Gly Pro Arg Gly	Pro Ala Gly Ala	Pro Gln Arg His Ser	
Leu Ser Glu	Ile Thr Tyr Leu	Gly Gln Pro Asp	Ile Ser Ile Leu Gln	
Pro Ser Asn	Val Pro Pro Pro	Gln Ile Leu Ser	Pro Leu Ser Tyr Ala	
Pro Asn Ala	Ala Pro Glu Val	Gly Pro Pro Ser	Tyr Ala Pro Gln Val	
Thr Pro Glu	Ala Gln Phe Pro	Phe Tyr Ala Pro	Gln Ala Ile Ser Lys	
Val Gln Pro	Ser Ser Tyr Ala	Pro Gln Ala Thr	Pro Asp Ser Trp Pro	
Pro Ser Tyr	Gly Val Cys Met	Glu Gly Ser Gly	Lys Asp Ser Pro Thr	
Gly Thr Leu	Ser Ser Pro Lys	His Leu Arg Pro	Lys Gly Gln Leu Gln	
Lys Glu Pro	Pro Ala Gly Ser	Cys Met Leu Gly	Gly Leu Ser Leu Gln	
Glu Val Thr	Ser Leu Ala Met	Glu Glu Ser Gln	Glu Ala Lys Ser Leu	
His Gln Pro	Leu Gly Ile Cys	Thr Asp Arg Thr	Ser Asp Pro Asn Val	
Leu His Ser	Gly Glu Glu Gly	Thr Pro Gln Tyr	Leu Lys Gly Gln Leu	
Pro Leu Leu	Ser Ser Val Gln	Ile Glu Gly His	Pro Met Ser Leu Pro	
Leu Gln Pro	Pro Ser Gly Pro	Cys Ser Pro Ser	Asp Gln Gly Pro Ser	
Pro Trp Gly	Leu Leu Glu Ser	Leu Val Cys Pro	Lys Asp Glu Ala Lys	
Ser Pro Ala	Pro Glu Thr Ser	Asp Leu Glu Gln	Pro Thr Glu Leu Asp	

Ser Leu Phe Arg Gly⁵ Leu Ala Leu Thr Val⁵ Gln Trp Glu Ser
565 570

<210> 3
<211> 211
<212> PRT
<213> Homo sapiens

<400> 3
Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
1 5 10 15
Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
20 25 30
Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
35 40 45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
50 55 60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65 70 75 80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
85 90 95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
100 105 110
Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
115 120 125
Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
130 135 140
Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145 150 155 160
His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
165 170 175
Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
180 185 190
Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
195 200 205
Thr Trp Thr
210

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu peptide tag

<400> 4
Glu Tyr Met Pro Met Glu
1 5

<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag-tag peptide

<400> 5
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 6
<211> 699
<212> DNA

<213> Homo sapiens

<400> 6

```

gagcccagat cttcagacaa aactcacaca tgccccaccgt gcccagcacc tgaagccgag 60
ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagtgc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctcttctctc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

```

<210> 7

<211> 1116

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (21)...(557)

<400> 7

```

tcgagttaga attgtctgca atg gcc gcc ctg cag aaa tct gtg agc tct ttc 53
                        Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe
                        1          5          10

ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg 101
Leu Met Gly Thr 15 Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu 25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agy ctt gac 149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp 30 35 40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg 197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu 45 50 55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att 245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile 60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
Gly Glu Lys Leu Phe 80 His Gly Val Ser Met 85 Ser Glu Arg Cys Tyr 90 Leu

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341
Met Lys Gln Val 95 Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln 100 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala 110 115 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu 125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu 140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe 160 165 170

```

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
 Met Ser Leu Arg Asn Ala Cys Ile
 175

taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
 aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
 tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag 767
 catagatatt tattgataac atttcattgt aactgggtgt ctatacacag aaaacaattt 827
 attttttaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
 aaacccctaa atagcttcat gtttccataa tcagtacttt atattttataa atgtatttat 947
 tattattata agactgcatt ttattttatat cattttatta atatggattt atttatagaa 1007
 acatcattcg atattgctac ttgagtgtaa ggctaataat gatatttatg acaataatta 1067
 tagagctata acatgtttat ttgacctcaa taaacacttg gatatccta 1116

<210> 8
 <211> 179
 <212> PRT
 <213> homo sapiens

<400> 8
 Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
 1 5 10 15
 Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Ala
 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide prime ZC28590

<400> 9
 ttgggtacct ctgcaatggc cgccctgcag aaatct 36

<210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide prime ZC28580

<400> 10
 ttgggatcca atgcaggcat ttctcagaga cat 33

<210> 11
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide prime ZC14666

<400> 11
 agccaccaag atgactga 18

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide prime ZC14742

<400> 12
 tgcatttggt aggtgcggtt ga 22

<210> 13
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His tag

<400> 13
 His His His His His His
 1 5

<210> 14
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC29239

<400> 14
 gaggccggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
 tgc 63

<210> 15
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC29232

<400> 15
 cgactgactc gagtcagtga tggatgatggt gatggccacc tgatccttta cccggagaca 60
 gggag 65

<210> 16
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC39319

<400> 16
 atcgaattc gcagaagcca tggcgtggag ccttggg 37

<210> 17
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC39325

<400> 17
 cagtggatcc ggaggggacc gtttcgtc 28

<210> 18
 <211> 660
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(660)

<400> 18
 atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca 48
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt 96
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg 144
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat 192
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc 240
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag 288
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att 336
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat 384
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc 624
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc 660
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 19
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 20
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC38931

<400> 20
 acaaagccgc gggaggag 18

<210> 21
 <211> 82
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC39042

<400> 21
 ctgactcgag tcagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca 60
 gtttacccgg agacagggag ag 82

<210> 22
 <211> 1428
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused
 to IgGg1 with a 6-HIS tag

<400> 22
 atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca 48
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Cys Leu Leu Val Ser
 1 5 10 15
 gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt 96
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg 144
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat 192
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc 240
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag 288
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att 336
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat 384
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc 624
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg 672
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
 210 215 220

12

ggt	tcg	ggt	tcg	gag	ccc	aga	tca	tca	gac	aaa	act	cac	aca	tgc	cca	720
Gly	Ser	Gly	Ser	Glu	Pro	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	
225					230					235					240	
ccg	tgc	cca	gca	cct	gaa	gcc	gag	ggg	gca	ccg	tca	gtc	ttc	ctc	ttc	768
Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	
				245					250					255		
ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	816
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
			260					265					270			
aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	864
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
		275					280					285				
aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	912
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
	290					295					300					
cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	960
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
305					310					315					320	
gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	1008
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
				325				330						335		
tcc	aac	aaa	gcc	ctc	cca	tcc	tcc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	1056
Ser	Asn	Lys	Ala	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
			340					345					350			
aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	1104
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
		355					360					365				
gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	1152
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
	370					375					380					
ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	1200
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
385					390					395					400	
gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	1248
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	
				405					410					415		
ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	1296
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	
			420					425					430			
ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	1344
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	
		435					440					445				
tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	ctg	gtt	ccg	cgt	1392
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Leu	Val	Pro	Arg	
	450					455					460					
ggt	tcc	gga	tca	ggt	ggc	cat	cac	cat	cac	cat	cac					1428
Gly	Ser	Gly	Ser	Gly	Gly	His	His	His	His	His	His					
465					470					475						

<210> 23
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
 210 215 220
 Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
 225 230 235 240
 Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
 245 250 255
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 260 265 270
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 275 280 285
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 290 295 300
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 305 310 315 320
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 325 330 335
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 340 345 350
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 355 360 365
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 370 375 380
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 385 390 395 400
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 405 410 415
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 420 425 430
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
 450 455 460
 Gly Ser Gly Ser Gly Gly His His His His His His
 465 470 475

<210> 24

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC29328

<400> 24

tcagagggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca 60
tgc 63

<210> 25

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC29231

<400> 25

cgactgactc gagctactcc ataggcatat actcgccacc tgatccttta cccggagaca 60
gggag 65

<210> 26

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC39335

<400> 26

atcggaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tgctcacgcc 70

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC28981

<400> 27

tttgggctcc ctgagctctg gtggaa 26

<210> 28

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC39043

<400> 28

ctgactcgag ctactccata ggcataact cgccacctga tccggaacca cgcggaacca 60
gtttaccgag agacaggag 80

<210> 29

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> hzcytor11 extracellular cytokine binding domain
fused to IgG1 with a Glu-Glu tag

<221> CDS

<222> (1)...(1452)

<400> 29

atg agg acg ctg ctg acc atc ttg act gtg gga tcc ctg gct gct cac 48
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His

1	5	10	15	15												
gcc Ala	cct Pro	gag Glu	gac Asp 20	ccc Pro	tcg Ser	gat Asp	ctg Leu	ctc Leu 25	cag Gln	cac His	gtg Val	aaa Lys	ttc Phe 30	cag Gln	tcc Ser	96
agc Ser	aac Asn	ttt Phe 35	gaa Glu	aac Asn	atc Ile	ctg Leu	acg Thr 40	tgg Trp	gac Asp	agc Ser	ggg Gly	cca Pro 45	gag Glu	ggc Gly	acc Thr	144
cca Pro	gac Asp 50	acg Thr	gtc Val	tac Tyr	agc Ser	atc Ile 55	gag Glu	tat Tyr	aag Lys	acg Thr	tac Tyr 60	gga Gly	gag Glu	agg Arg	gac Asp	192
tgg Trp 65	gtg Val	gca Ala	aag Lys	aag Lys	ggc Gly 70	tgt Cys	cag Gln	cgg Arg	atc Ile	acc Thr 75	cgg Arg	aag Lys	tcc Ser	tgc Cys	aac Asn 80	240
ctg Leu	acg Thr	gtg Val	gag Glu	acg Thr 85	ggc Gly	aac Asn	ctc Leu	acg Thr	gag Glu 90	ctc Leu	tac Tyr	tat Tyr	gcc Ala	agg Arg 95	gtc Val	288
acc Thr	gct Ala	gtc Val	agt Ser 100	gcg Ala	gga Gly	ggc Gly	cgg Arg	tca Ser 105	gcc Ala	acc Thr	aag Lys	atg Met	act Thr 110	gac Asp	agg Arg	336
ttc Phe	agc Ser	tct Ser 115	ctg Leu	cag Gln	cac His	act Thr	acc Thr 120	ctc Leu	aag Lys	cca Pro	cct Pro	gat Asp 125	gtg Val	acc Thr	tgt Cys	384
atc Ile 130	tcc Ser	aaa Lys	gtg Val	aga Arg	tcg Ser	att Ile 135	cag Gln	atg Met	att Ile	gtt Val 140	cat His	cct Pro	acc Thr	ccc Pro	acg Thr	432
cca Pro 145	atc Ile	cgt Arg	gca Ala	ggc Gly	gat Asp 150	ggc Gly	cac His	cgg Arg	cta Leu	acc Thr 155	ctg Leu	gaa Glu	gac Asp	atc Ile	ttc Phe 160	480
cat His	gac Asp	ctg Leu	ttc Phe	tac Tyr 165	cac His	tta Leu	gag Glu	ctc Leu	cag Gln 170	gtc Val	aac Asn	cgc Arg	acc Thr	tac Tyr 175	caa Gln	528
atg Met	cac His	ctt Leu	gga Gly 180	ggg Gly	aag Lys	cag Gln	aga Arg	gaa Glu 185	tat Tyr	gag Glu	ttc Phe	ttc Phe	ggc Gly 190	ctg Leu	acc Thr	576
cct Pro	gac Asp	aca Thr 195	gag Glu	ttc Phe	ctt Leu	ggc Gly	acc Thr 200	atc Ile	atg Met	att Ile	tgc Cys	gtt Val 205	ccc Pro	acc Thr	tgg Trp	624
gcc Ala	aag Lys 210	gag Glu	agt Ser	gcc Ala	ccc Pro	tac Tyr 215	atg Met	tgc Cys	cga Arg	gtg Val	aag Lys 220	aca Thr	ctg Leu	cca Pro	gac Asp	672
cgg Arg 225	aca Thr	tgg Trp	acc Thr	gga Gly	tcc Ser 230	ggt Gly	tcg Ser	ggt Gly	tcg Ser	ggt Gly 235	tcg Ser	gag Glu	ccc Pro	aga Arg	tca Ser 240	720
tca Ser	gac Asp	aaa Lys	act Thr	cac His 245	aca Thr	tgc Cys	cca Pro	ccg Pro	tgc Cys 250	cca Pro	gca Ala	cct Pro	gaa Glu	gcc Ala 255	gag Glu	768
ggg Gly	gca Ala	ccg Pro	tca Ser 260	gtc Val	ttc Phe	ctc Leu	ttc Phe	ccc Pro 265	cca Pro	aaa Lys	ccc Pro	aag Lys	gac Asp 270	acc Thr	ctc Leu	816
atg Met	atc Ile	tcc Ser 275	cgg Arg	acc Thr	cct Pro	gag Glu	gtc Val 280	aca Thr	tgc Cys	gtg Val	gtg Val	gtg Val 285	gac Asp	gtg Val	agc Ser	864

cac His	gaa Glu	gac Asp	cct Pro	gag Glu	gtc Val	aag Lys	ttc Phe	aac Asn	tgg Trp	tac Tyr	gtg Val	gac Asp	ggc Gly	gtg Val	gag Glu	912
	290					295					300					
gtg Val	cat His	aat Asn	gcc Ala	aag Lys	aca Thr	aag Lys	ccg Pro	cgg Arg	gag Glu	gag Glu	cag Gln	tac Tyr	aac Asn	agc Ser	acg Thr	960
305					310					315					320	
tac Tyr	cgt Arg	gtg Val	gtc Val	agc Ser	gtc Val	ctc Leu	acc Thr	gtc Val	ctg Leu	cac His	cag Gln	gac Asp	tgg Trp	ctg Leu	aat Asn	1008
				325					330					335		
ggc Gly	aag Lys	gag Glu	tac Tyr	aag Lys	tgc Cys	aag Lys	gtc Val	tcc Ser	aac Asn	aaa Lys	gcc Ala	ctc Leu	cca Pro	tcc Ser	tcc Ser	1056
			340					345					350			
atc Ile	gag Glu	aaa Lys	acc Thr	atc Ile	tcc Ser	aaa Lys	gcc Ala	aaa Lys	ggg Gly	cag Gln	ccc Pro	cga Arg	gaa Glu	cca Pro	cag Gln	1104
		355					360					365				
gtg Val	tac Tyr	acc Thr	ctg Leu	ccc Pro	cca Pro	tcc Ser	cgg Arg	gat Asp	gag Glu	ctg Leu	acc Thr	aag Lys	aac Asn	cag Gln	gtc Val	1152
	370					375					380					
agc Ser	ctg Leu	acc Thr	tgc Cys	ctg Leu	gtc Val	aaa Lys	ggc Gly	ttc Phe	tat Tyr	ccc Pro	agc Ser	gac Asp	atc Ile	gcc Ala	gtg Val	1200
385					390					395					400	
gag Glu	tgg Trp	gag Glu	agc Ser	aat Asn	ggg Gly	cag Gln	ccg Pro	gag Glu	aac Asn	aac Asn	tac Tyr	aag Lys	acc Thr	acg Thr	cct Pro	1248
				405					410					415		
ccc Pro	gtg Val	ctg Leu	gac Asp	tcc Ser	gac Asp	ggc Gly	tcc Ser	ttc Phe	ttc Phe	ctc Leu	tac Tyr	agc Ser	aag Lys	ctc Leu	acc Thr	1296
			420					425					430			
gtg Val	gac Asp	aag Lys	agc Ser	agg Arg	tgg Trp	cag Gln	cag Gln	ggg Gly	aac Asn	gtc Val	ttc Phe	tca Ser	tgc Cys	tcc Ser	gtg Val	1344
		435					440					445				
atg Met	cat His	gag Glu	gct Ala	ctg Leu	cac His	aac Asn	cac His	tac Tyr	acg Thr	cag Gln	aag Lys	agc Ser	ctc Leu	tcc Ser	ctg Leu	1392
	450					455					460					
tct Ser	ccg Pro	ggt Gly	aaa Lys	ctg Leu	gtt Val	ccg Pro	cgt Arg	ggt Gly	tcc Ser	gga Gly	tca Ser	ggt Gly	ggc Gly	gag Glu	tat Tyr	1440
465					470				475						480	
atg Met	cct Pro	atg Met	gag Glu													1452

<210> 30

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide encoded by the hzcytor11 extracellular
cytokine binding domain fused to IgGg1 with a
Glu-Glu tag of SEQ ID NO: 29

<400> 30

Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His
1				5					10				15		
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser
			20					25					30		

17

Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr
		35					40					45			
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp
	50					55					60				
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn
65					70					75					80
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val
				85					90					95	
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg
			100					105					110		
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys
		115					120					125			
Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr
	130					135					140				
Pro	Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe
145					150					155					160
His	Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln
				165					170					175	
Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr
			180					185					190		
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp
		195					200					205			
Ala	Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp
	210					215					220				
Arg	Thr	Trp	Thr	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Glu	Pro	Arg	Ser
225					230					235					240
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu
				245					250					255	
Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			260					265					270		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
		275					280					285			
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
	290					295					300				
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
305					310					315					320
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
				325					330					335	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ser	Ser
			340					345					350		
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
		355					360					365			
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
	370					375					380				
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
385					390					395					400
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
				405					410					415	
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
			420					425					430		
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
		435					440					445			
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
	450					455					460				
Ser	Pro	Gly	Lys	Leu	Val	Pro	Arg	Gly	Ser	Gly	Ser	Gly	Gly	Glu	Tyr
465					470					475					480
Met	Pro	Met	Glu												

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC37693

<400> 31

ccccagacac ggtctacagc at

22

<210> 32
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC37449

<400> 32
 gggtcaggcc gaagaactca tat

23

<210> 33
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
 1 5 10 15
 Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr
 20 25 30
 Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

<210> 34
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 34
 Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
 1 5 10 15
 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
 20 25 30
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125

Arg	Pro	Lys	Met	Ala	Pro	Ala	Ash	Asp	Thr	Tyr	Glu	Ser	Ile	Phe	Ser
	130					135				19	140				
His	Phe	Arg	Glu	Tyr	Glu	Ile	Ala	Ile	Arg	Lys	Val	Pro	Gly	Asn	Phe
145					150					155					160
Thr	Phe	Thr	His	Lys	Lys	Val	Lys	His	Glu	Asn	Phe	Ser	Leu	Leu	Thr
				165					170					175	
Ser	Gly	Glu	Val	Gly	Glu	Phe	Cys	Val	Gln	Val	Lys	Pro	Ser	Val	Ala
			180					185					190		
Ser	Arg	Ser	Asn	Lys	Gly	Met	Trp	Ser	Lys	Glu	Glu	Cys	Ile	Ser	Leu
		195					200					205			
Thr	Arg	Gln													
	210														

<210> 35
 <211> 201
 <212> PRT
 <213> Homo sapiens

Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser
1				5					10					15	
Thr	Asn	Met	Lys	His	Ile	Ile	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly
			20					25					30		
Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu
		35					40					45			
Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu
	50					55					60				
Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr
65					70				75						80
Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser
				85					90					95	
Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	Thr	Ile	Leu	Thr	Arg	Pro
			100					105					110		
Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	His	Leu	Val	Ile	Glu	Leu	Glu
	115						120					125			
Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu
	130					135					140				
Pro	Gly	Ala	Glu	Glu	His	Val	Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro
145					150					155					160
Val	His	Leu	Glu	Thr	Met	Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala
				165					170					175	
Gln	Thr	Phe	Val	Lys	Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr
			180					185					190		
Glu	Cys	Val	Glu	Val	Gln	Gly	Glu	Ala							
		195					200								